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Pairwise approximation for *SIR* type network epidemics with non-Markovian recovery

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We present the generalised mean-field and pairwise models for non-Markovian epidemics on networks with arbitrary recovery time distributions. First we consider a hyperbolic partial differential equation (PDE) system, where the population of infective nodes and links are structured by age since infection. We show that the PDE system can be reduced to a system of integro-differential equations, which is analysed analytically and numerically. We investigate the asymptotic behaviour of the generalised model and provide an implicit analytical expression involving the final epidemic size and pairwise reproduction number. As an illustration of the applicability of the general model, we recover known results for the exponentially distributed and fixed recovery time cases. For gamma- and uniformly-distributed infectious periods, new pairwise models are derived. Theoretical findings are confirmed by comparing results from the new pairwise model and explicit stochastic network simulation. A major benefit of the generalised pairwise model lies in approximating the time evolution of the epidemic.

1. Introduction

It has long been acknowledged that the connectivity pattern between individuals in a population is an important factor in determining how diseases invade, spread or how to design or deploy optimal control measures [4,14,18,24,25]. Using networks to model disease transmission, individuals can be represented by nodes in a network and the connectivity between individuals can be represented by links between the

nodes. This allows modellers to capture a high level of detail of many realistic contact processes. In this framework we can develop more accurate models, especially when compared to classical compartmental models which usually operate on the assumption of homogeneous random mixing. The most popular node-level models are perhaps the degree-based or heterogeneous mean-field models. The pairwise models offer an explicit treatment of the epidemic process both at node and link level [15,19]. Such and other models of epidemic dynamics of networks (see [31] for a review) have led to a much better understanding of the role of contact heterogeneity, assortativity and clustering of contacts. While networks deal with the complexity of the contact structure, epidemic models on networks often only consider Markovian transmission and recovery processes. However, empirical observations show that assuming Markovian infectiousness is a strong simplifying assumption [16,21]. Unfortunately, the analysis of non-Markovian systems is significantly more challenging and requires deeper theoretical and numerical tools. This paper is motivated by the renewed interest in non-Markovian processes [5,8,12,23] and aims to extend the pairwise model from Markovian to non-Markovian epidemics, where the infection process is Markovian but the infectious period is taken from an arbitrary distribution.

Research in this area is based on different mathematical techniques depending on how the exact stochastic process is approximated. If the main focus is on the early (i.e. epidemic threshold) and asymptotic behaviour (i.e. final epidemic size) of the epidemic, then probabilistic models based on branching process approximations and susceptibility sets as well as percolation models can provide analytical results. In these cases the impact of the network structure on the epidemic threshold and final epidemic size is clear. For example, in [2] the final epidemic size is given implicitly by an equation connecting it to moments of the network degree and other factors. The percolation-theory-based approach [17,27] applies even more widely for general transmission and recovery processes. It provides implicit analytical equations which determine the final epidemic size and links it to average characteristics of the epidemic process (e.g. transmissibility) and network properties (e.g. 1st and 2nd moment of the degree distribution). However, both approaches fail to characterise the time-evolution of the epidemic.

The message passing approach [13,45] is also an effective way to model an epidemic with arbitrary transmission and recovery processes, but at the expense of a system consisting of a large number of integro-differential equations. By using the concept of average message, one can further simplify the equations and gain insight into both the time evolution of the epidemic and final epidemic size. Edge-based compartmental models [29] have also been successful in capturing SIR dynamics on configuration-like networks and for Markovian models, giving perhaps the most compact ODE models that provide an excellent approximation of the exact stochastic network epidemic. They become exact in some appropriate limits and conditions on the underlying network [3,9,11]. The overwhelming view is that such models complement each other and offer a different or complimentary perspective of the exact stochastic process. Often it turns out that such models are in fact equivalent in some well defined sense or limit [30,41], and they all contribute to a better or more complete understanding of exact stochastic processes on networks.

For the Markovian case, the pairwise model is amenable to extensions to either networks with more exotic properties, such as directed [35] and weighted [33] networks. Here we focus on generalising this approach to the case of non-Markovian epidemics and test the flexibility of this modelling framework. This paper is structured as follows: in Section 2, we present the derivation of pairwise and mean-field models for arbitrary infectious periods, with the most technical part of the calculations presented in the Appendix. Section 3 includes the mathematical analysis of the resulting systems, with focus on the positivity of solutions, associated reproduction numbers and the implicit relation concerning the final epidemic size. In Section 4 we illustrate that in special cases the resulting system can be reduced to the well-known and previously studied models. In the Appendix we collect the most technical parts of proofs, namely the calculations involved in the model derivation and the algebraic manipulations of the resulting multiple integrals.

2. Model derivation

We consider an undirected and unweighted regular network with N nodes where each node has n link/edges. For our purposes such networks would be created using the configuration model with clustering going to zero as the network size increases. However, we note that our results will remain valid for Erdős-Rényi random networks as well. Each node has a state at any time t , which can be susceptible (S), infected (I) or recovered (R). If an infection happens along an $S - I$ link, then the state of the susceptible node S changes to I . Each infected node has infectious period chosen from some given distribution and after it elapses, the node recovers and changes its state to R permanently, which means that the infectious period is the same as the recovery time and recovered nodes remain immune.

We want to build mean-field and pairwise models for the SIR epidemic process with Markovian transmission (i.e. time to infection is exponentially distributed) and general recovery time distribution. We use the notations $[X](t)$, $[XY](t)$ and $[XYZ](t)$ to denote the expected number of nodes in state X , links in state $X - Y$ and triples in state $X - Y - Z$, respectively, where $X, Y, Z \in \{S, I, R\}$. For the derivation of a model at the level of nodes (i.e. for mean-field model), we obtain equations for $[\dot{S}](t)$ and $[\dot{I}](t)$, and these depend on the expected number of pairs. For the pairwise model (at the level of links/pairs) equations for $[\dot{S}S](t)$ and $[\dot{S}I](t)$ are needed, which in turn depend on triples.

First, let $i(t, a)$ represent the density of infected nodes with respect to the age of infection a at the current time t , then $[I](t) = \int_0^\infty i(t, a) da$. Similarly, $Si(t, a)$ and $ISI(t, a)$ describe the density of $S - i$ links and $I - S - i$ triplets, respectively, where the infected node i has age a at time t and $[SI](t) = \int_0^\infty Si(t, a) da$, $[ISI](t) = \int_0^\infty ISI(t, a) da$. We assume that the infection process along $S - I$ links is Markovian with transmission rate $\tau > 0$. The recovery part is considered to be non-Markovian, with a cumulative distribution function $F(a)$ and probability density function $f(a)$. We use the associated survival function $\xi(a) = 1 - F(a)$ and hazard function $h(a) = -\frac{\xi'(a)}{\xi(a)} = \frac{f(a)}{\xi(a)}$.

Using the notations above, we arrive at the following model

$$[\dot{S}](t) = -\tau[SI](t), \quad (2.1a)$$

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) i(t, a) = -h(a)i(t, a), \quad (2.1b)$$

$$[\dot{S}S](t) = -2\tau[SSI](t), \quad (2.1c)$$

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a}\right) Si(t, a) = -\tau ISI(t, a) - (\tau + h(a))Si(t, a), \quad (2.1d)$$

subject to the boundary conditions

$$i(t, 0) = \tau[SI](t), \quad (2.2a)$$

$$Si(t, 0) = \tau[SSI](t), \quad (2.2b)$$

and initial conditions

$$[S](0) = [S]_0, \quad [SS](0) = [SS]_0, \quad i(0, a) = \varphi(a), \quad (2.3a)$$

$$Si(0, a) = \chi(a) \approx \frac{n}{N} [S]_0 i(0, a) = \frac{n}{N} [S]_0 \varphi(a). \quad (2.3b)$$

We shall use the biologically feasible assumption $\lim_{a \rightarrow \infty} \varphi(a) = 0$. To break the dependence on higher order moments, we apply the closure approximation formula, as given in [32] (see section 2 (a) for further details),

$$[XSY](t) = \frac{n-1}{n} \frac{[XS](t)[SY](t)}{[S](t)}, \quad (2.4)$$

which can be also applied for $XSi(t, a)$ in the form

$$XSi(t, a) = \frac{n-1}{n} \frac{[XS](t)Si(t, a)}{[S](t)}, \quad X \in \{S, I\}. \quad (2.5)$$

To obtain a self-consistent system in terms of network-level averaged quantities such as $[S]$, $[SS]$, $[I]$ and $[SI]$, further calculations are needed, which are presented in Appendix (a). The resulting pairwise system is the following integro-differential equation:

$$[\dot{S}](t) = -\tau[SI](t) \quad (2.6a)$$

$$[\dot{SS}](t) = -2\tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} \quad (2.6b)$$

$$[\dot{I}](t) = \tau[SI](t) - \int_0^t \tau[SI](t-a)f(a)da - \int_t^\infty \varphi(a-t) \frac{f(a)}{\xi(a-t)} da \quad (2.6c)$$

$$\begin{aligned} [\dot{SI}](t) = & \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)} [SI](t) - \tau[SI](t) \\ & - \int_0^t \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} e^{-\int_{t-a}^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} f(a) da \\ & - \int_t^\infty \frac{n}{N} [S]_0 \varphi(a-t) e^{-\int_0^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} \frac{f(a)}{\xi(a-t)} da. \end{aligned} \quad (2.6d)$$

From Eq. (2.6), the associated mean-field model can be easily deduced by using the closure approximation formula for homogeneous networks (i.e. n -regular graphs)

$$[XY](t) = \frac{n}{N} [X](t)[Y](t), \quad (2.7)$$

thus the node-level system becomes

$$\dot{S}(t) = -\tau \frac{n}{N} S(t)I(t) \quad (2.8a)$$

$$\dot{I}(t) = \tau \frac{n}{N} S(t)I(t) - \int_0^t \tau \frac{n}{N} S(t-a)I(t-a)f(a)da - \int_t^\infty \varphi(a-t) \frac{f(a)}{\xi(a-t)} da. \quad (2.8b)$$

In the following, we investigate these systems from mathematical and numerical point of view, focussing on the epidemiologically meaningful properties of the models.

(a) The relation of the stochastic and mean-field epidemic model

The underlying epidemic model is a stochastic model unfolding on a network of N nodes with three possible states (S, I, R). When the transmission and the recovery processes are Markovian, the corresponding 3^N forward Kolmogorov equations make the analysis of the model extremely difficult. Starting at the microscopic level and seeking to derive a meaningful mean-field model relies on considering the expected values of some appropriately chosen random variables. In the case of the pairwise model these are the expected number of singles, pairs and triples of appropriate types. However, developing limiting mean-field models (be these ordinary or integro-differential equation) for these usually rely on higher order moments or correlations between these random variables. In kinetic theory the propagation of chaos or mean-field particle methods essentially relies on assuming independence, e.g. the expected value of a product of random variables is equal to the product of the expectations [40], this in our case translates to assuming that the expected number of triples can be approximated in terms of the expected number of pairs and singles. This was shown in [32] by assuming a regular network and that the states of nodes around a given susceptible node are multinomially distributed with probabilities depending on the expected number of pairs and singles alone. While here we do not provide a rigorous proof that our model is a large-scale limiting model of the stochastic process, numerical tests confirm the validity of our model, see Fig. 1.

Perhaps related but more widely used in the mathematical-biology community are the formal proofs by Decreusefond et al. [9], Barbour and Reinert [3] and Janson et al. [11] which are all concerned with the limiting mean-field equations of the SIR stochastic epidemic on configuration networks. Decreusefond et al. [9] study a measure-valued process capturing the degrees of susceptible individuals and the number of edges between different types of nodes. They prove that, as $N \rightarrow \infty$, the measure-valued process converges to a deterministic limit, from which the Volz [43] equations may be derived as a corollary.

Barbour and Reinert [3] use multitype branching process approximations to prove results approximating the entire course of an SIR epidemic within a more general non-Markovian framework, allowing degree dependent infection and recovery time distributions. Janson et al. [11] relaxes some of the conditions on the degree distribution.

These are strong theoretical results which cement many empirical observations and numerical validations, and such a type of proof in our case is beyond the scope of our paper. In our paper the derivation of the model is intuitive and its validation is done numerically. However, pairwise models before a closure and for Markovian epidemics have been proved to be exact [42]. Moreover, it is possible that the validity of our model could be established more rigorously using the results in [3] augmented by the argument that the Volz-type and pairwise equations are equivalent [18,30].

3. General results

In this section, we explore the most important features of systems (2.6) and (2.8). First, we find a first integral of the pairwise model (2.6), which allows us to reduce the dimensionality. We show that the solutions of the models are biologically meaningful, i.e. solutions with nonnegative data remain nonnegative for $t \geq 0$. The central result of this part is the implicit relation between the reproduction number and the final epidemic size. We summarise the definitions of the associated reproduction numbers referring to [19], where the basic (\mathcal{R}_0) and pairwise (\mathcal{R}_0^p) reproduction numbers are precisely introduced for mean-field and pairwise models, respectively.

(a) First integral

We use (2.6a) and (2.6b) to find an invariant quantity of the system.

Proposition 3.1. *The function $U(t) = \frac{[SS](t)}{[S]^{2\frac{n-1}{n}}(t)}$ is a first integral of system (2.6).*

Proof. To see this, let us divide Eq. (2.6b) by Eq. (2.6a), which gives

$$\frac{d[SS]}{d[S]} = \frac{-2\tau\frac{n-1}{n}\frac{[SS][SI]}{[S]}}{-\tau[SI]} = 2\frac{n-1}{n}\frac{[SS]}{[S]}.$$

Solving this equation, we find $[SS] = K[S]^{2\frac{n-1}{n}}$, where K is a constant, thus $U(t) = \frac{[SS](t)}{[S]^{2\frac{n-1}{n}}(t)}$ is an invariant quantity in the system and its value is

$$U(0) = K = \frac{[SS](0)}{[S]^{2\frac{n-1}{n}}(0)} = \frac{[SS]_0}{[S]_0^{2\frac{n-1}{n}}} = \frac{n[S]_0\frac{[S]_0}{N}}{[S]_0^{2\frac{n-1}{n}}} = \frac{n}{N}[S]_0^{\frac{2}{n}}.$$

□

Consequently, using this first integral, we obtain

$$[SS](t) = \frac{n}{N}[S]_0^{\frac{2}{n}}[S]^{2\frac{n-1}{n}}(t). \quad (3.1)$$

Applying Eq. (3.1), we can reduce our pairwise model to a two-dimensional system:

$$\begin{aligned}\dot{[S]}(t) &= -\tau[S I](t), \\ \dot{[S I]}(t) &= \tau\kappa[S]^{\frac{n-2}{n}}(t)[S I](t) - \tau[S I](t) - \tau\frac{n-1}{n}\frac{[S I](t)}{[S](t)}[S I](t) \\ &\quad - \int_0^t \tau\kappa[S]^{\frac{n-2}{n}}(t-a)[S I](t-a)e^{-\int_{t-a}^t \tau\frac{n-1}{n}\frac{[S I](s)}{[S](s)} + \tau ds} f(a) da \\ &\quad - \int_t^\infty \frac{n}{N}[S]_0 \varphi(a-t)e^{-\int_0^t \tau\frac{n-1}{n}\frac{[S I](s)}{[S](s)} + \tau ds} \frac{f(a)}{\xi(a-t)} da,\end{aligned}\quad (3.2)$$

where

$$\kappa = \frac{n-1}{N}[S]_0^{\frac{2}{n}}.$$

(b) Positivity

We are interested only in nonnegative solutions of system (2.6). The following proposition shows, that the solutions remain nonnegative provided that the initial conditions are nonnegative.

Proposition 3.2. *If initial conditions $[S]_0, [SS]_0$ are nonnegative and $\varphi(a) \geq 0$ for $a \geq 0$, then $[S](t) \geq 0$, $[SS](t) \geq 0$, $[I](t) \geq 0$ and $[S I](t) \geq 0$ hold for $t \geq 0$.*

Proof. It is clear, that $[SS](t)$ remains nonnegative, if the initial condition $[SS](0)$ is nonnegative, because $[SS](t)$ can be expressed from Eq. (2.6b) in the form

$$[SS](t) = [SS]_0 e^{-2\tau\frac{n-1}{n}\int_0^t \frac{[S I](s)}{[S](s)} ds}.$$

Moreover, if $[SS]_0$ is positive, then $[SS](t) > 0$ for all $t \geq 0$. From Eq. (3.1) we obtain that $[S](t)$ cannot be zero, if $[SS](t)$ is positive for all $t \geq 0$, which implies (from continuity of solutions) $[S](t) > 0$ for $t \geq 0$. From the derivation of system (2.6) (see Appendix), we have the following formulae for $[I](t)$ and $[S I](t)$:

$$[I](t) = \int_0^t \tau[S I](t-a)\xi(a)da + \int_t^\infty \varphi(a-t)\frac{\xi(a)}{\xi(a-t)}da,\quad (3.3)$$

and

$$\begin{aligned}[S I](t) &= \int_0^t \tau\frac{n-1}{n}\frac{[SS](t-a)[S I](t-a)}{[S](t-a)}e^{-\int_{t-a}^t \tau\frac{n-1}{n}\frac{[S I](s)}{[S](s)} + \tau ds}\xi(a)da \\ &\quad + \int_t^\infty \frac{n}{N}[S]_0\varphi(a-t)e^{-\int_0^t \tau\frac{n-1}{n}\frac{[S I](s)}{[S](s)} + \tau ds}\frac{\xi(a)}{\xi(a-t)}da.\end{aligned}\quad (3.4)$$

It can be seen that $[I](t)$ remains nonnegative if $[S I](t)$ is nonnegative for $t \geq 0$. On the other hand, $[S I](t_0)$ cannot be zero for some $t_0 \geq 0$, because the right-hand side of (3.4) depends on the $[S](t; t < t_0)$, $[SS](t; t < t_0)$ and $[S](t; t < t_0)$, which are positive, hence $[S I](t) > 0$. \square

In the case of the mean-field model (2.8), the positivity of $S(t)$ is clear. To see the positivity of $I(t)$, we substitute (2.7) into (3.3), which gives

$$I(t) = \int_0^t \tau\frac{n}{N}S(t-a)I(t-a)\xi(a)da + \int_t^\infty \varphi(a-t)\frac{\xi(a)}{\xi(a-t)}da.\quad (3.5)$$

Notice that $I(t)$ remains nonnegative if $S(t)$ is nonnegative for $t \geq 0$.

(c) Reproduction numbers \mathcal{R}_0 and \mathcal{R}_0^p

To determine the reproduction numbers for our models, we start with the usual interpretation, which specifies \mathcal{R}_0 as the number of secondary infections generated by a ‘typical’ infected individual introduced into a fully susceptible population during its infectious period. In [19] the

reproduction numbers are precisely described in both cases: in context of mean-field model, we use the *basic* reproduction number \mathcal{R}_0 , which is the expected lifetime of an I node multiplied by the number of newly generated I nodes per unit time. On the other hand, the *pairwise* reproduction number \mathcal{R}_0^p is the expected lifetime of an $S-I$ link multiplied by the number of newly generated $S-I$ links per unit time. These definitions above give

$$\mathcal{R}_0 = \tau[SI]_0 \mathbb{E}(\mathcal{I}), \quad (3.6)$$

where $\mathbb{E}(\mathcal{I})$ denotes the expected value of the random variable \mathcal{I} defined by the infectious period of an infected node, and

$$\mathcal{R}_0^p = \tau[SSI]_0 \mathbb{E}(\mathcal{Z}) = \tau[SSI]_0 \frac{(1 - \mathcal{L}[f](\tau))}{\tau}, \quad (3.7)$$

where $\mathbb{E}(\mathcal{Z})$ denotes the expected value of the random variable \mathcal{Z} defined by the lifetime of an $S-I$ link and $\mathcal{L}[f](\tau)$ denotes the Laplace transform of f , the density of the recovery process at τ . Applying the mean-field closure assumption (2.7) for (3.7), we get

$$\mathcal{R}_0 = \tau \frac{n}{N} S_0 \mathbb{E}(\mathcal{I}), \quad (3.8)$$

and using the pairwise closure approximation (2.4) and first integral (3.1) in (3.7), we find

$$\mathcal{R}_0^p = \frac{n-1}{N} [S]_0 (1 - \mathcal{L}[f](\tau)). \quad (3.9)$$

We omit the detailed calculations here (see [19]). Note that while in compartmental models \mathcal{R}_0 can be interpreted as the growth factor of subsequent generations of infected individuals in the initial phase of the epidemic, \mathcal{R}_0^p in the pairwise model can intuitively be understood as the growth factor of subsequent generations of infected links. The well known form of the basic reproduction number for stochastic epidemics on networks is [22]

$$\mathcal{R}_0^s = T \left(\frac{\langle k^2 \rangle - \langle k \rangle}{\langle k \rangle} \right), \quad (3.10)$$

where T is the average transmissibility, and $\langle k \rangle$ and $\langle k^2 \rangle$ are the first and second moment of the network's degree distribution. In our case $\langle k \rangle = n$, $\langle k^2 \rangle = n^2$, and $T = 1 - \mathcal{L}[f](\tau)$. The latter equality can be seen as follows: consider an isolated $S-I$ link, and let \mathcal{E} be the exponentially distributed random variable of the time of infection along this link, with parameter τ . Then the probability of transmission is the same as the probability that infection occurs before recovery, that is

$$T = P(\mathcal{E} < \mathcal{I}) = \int_0^\infty F_{\mathcal{E}}(y) f(y) dy = \int_0^\infty (1 - e^{-\tau y}) f(y) dy = 1 - \mathcal{L}[f](\tau). \quad (3.11)$$

Hence,

$$\mathcal{R}_0^p = \frac{n-1}{N} [S]_0 (1 - \mathcal{L}[f](\tau)) \underset{[S]_0 \rightarrow N}{\simeq} (1 - \mathcal{L}[f](\tau)) \left(\frac{n^2 - n}{n} \right) = \mathcal{R}_0^s, \quad (3.12)$$

and thus the two approaches are equivalent. The intuitive derivation for \mathcal{R}_0^p follows from considering the rate at which new $S-I$ links are created. From (2.6d), and focusing on the single positive term on the right hand side, it follows that $S-I$ links are created at rate $\frac{\tau(n-1)}{n} \frac{[SS]}{[S]}$ which at time $t=0$ and with a vanishingly small initial number of infected nodes reduces to $\tau(n-1)$. Now, multiplying this by the average lifetime of an $S-I$ link, which is $\mathbb{E}(\mathcal{Z}) = \frac{1 - \mathcal{L}[f](\tau)}{\tau}$, gives the desired threshold value in the limit of $[S] \rightarrow N$ at $t=0$.

(d) Final size relation

In this part, we derive final size relations that allow us to calculate the total number of infected nodes during an epidemic outbreak on the network. We use the notation $s_\infty = \frac{[S]_\infty}{[S]_0}$, where $[S]_\infty = \lim_{t \rightarrow \infty} [S](t)$ and $1 - s_\infty$ is called the attack rate (the fraction of infected nodes).

Theorem 3.1. *The final size relation associated to the mean-field model (2.8) is*

$$\ln(s_\infty) = \mathcal{R}_0(s_\infty - 1), \quad (3.13)$$

where the basic reproduction number \mathcal{R}_0 is defined in (3.8).

Proof. From (2.8a), we obtain

$$S_\infty - S_0 = -\tau \frac{n}{N} \int_0^\infty S(u)I(u)du \quad (3.14)$$

and

$$\ln\left(\frac{S_\infty}{S_0}\right) = -\tau \frac{n}{N} \int_0^\infty I(u)du. \quad (3.15)$$

Substituting (3.5) into (3.15), we get

$$\begin{aligned} \ln\left(\frac{S_\infty}{S_0}\right) &= -\tau \frac{n}{N} \int_0^\infty \int_0^u \tau \frac{n}{N} S(u-a)I(u-a)\xi(a)dadu \\ &\quad -\tau \frac{n}{N} \int_0^\infty \int_u^\infty \varphi(a-u) \frac{\xi(a)}{\xi(a-u)} dadu. \end{aligned}$$

Neglecting the small number of initial infecteds ($\varphi(a) \approx 0$), we obtain

$$\ln\left(\frac{S_\infty}{S_0}\right) = -\left(\tau \frac{n}{N}\right)^2 \int_0^\infty \int_0^u S(u-a)I(u-a)\xi(a)dadu. \quad (3.16)$$

After some algebraic manipulation (for details, see Appendix (b)), we obtain

$$\ln\left(\frac{S(\infty)}{S(0)}\right) = \tau \frac{n}{N} \mathbb{E}(\mathcal{I})(S(\infty) - S(0)), \quad (3.17)$$

where \mathcal{I} denotes the infectious period of an infected node. Therefore, we found (3.13). \square

We note that in [6] a similar calculation has been performed to derive the final size relation for an age-of-infection model. In the following, we derive our main mathematical result that is the final-size relation for the pairwise system (2.6).

Theorem 3.2. *The final size relation associated to the pairwise model (2.6) is*

$$\frac{s_\infty^{\frac{1}{n}} - 1}{\frac{1}{n-1}} = \mathcal{R}_0^p \left(s_\infty^{\frac{n-1}{n}} - 1 \right), \quad (3.18)$$

where the pairwise reproduction number \mathcal{R}_0^p is defined in (3.9).

Proof. The second equation of the two-dimensional system (3.2) has the general form

$$x'(t) = \alpha(t) - \beta(t)x(t),$$

where

$$\begin{aligned} \alpha(c) &= \tau \kappa[S]^{\frac{n-2}{n}}(c)[SI](c) \\ &\quad - \int_0^c \tau \kappa[S]^{\frac{n-2}{n}}(c-a)[SI](c-a)f(a)e^{-\int_{c-a}^c \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} da \\ &\quad - \int_c^\infty \frac{n}{N} [S]_0 \varphi(a-c) \frac{f(a)}{\xi(a-c)} e^{-\int_0^c \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} da, \\ \beta(w) &= \tau + \tau \frac{n-1}{n} \frac{[SI](w)}{[S](w)}, \\ x(t) &= [SI](t), \end{aligned}$$

and has the solution

$$x(u) = e^{-\int_0^u \beta(w)dw} x(0) + \int_0^u e^{-\int_c^u \beta(w)dw} \alpha(c)dc. \quad (3.19)$$

Using (2.1a), simple calculations give the relations

$$\begin{aligned} e^{-\int_0^u \tau + \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} ds} &= e^{-\tau u} \frac{[S]^{\frac{n-1}{n}}(u)}{[S]^{\frac{n-1}{n}}(0)}, \\ e^{-\int_c^u \tau + \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} ds} &= e^{-\tau(u-c)} \frac{[S]^{\frac{n-1}{n}}(u)}{[S]^{\frac{n-1}{n}}(c)}. \end{aligned}$$

Using these relations, from (3.19) we get

$$\begin{aligned} [SI](u) &= \frac{[SI](0)}{[S]^{\frac{n-1}{n}}(0)} e^{-\tau u} [S]^{\frac{n-1}{n}}(u) + \int_0^u \tau \kappa [S]^{-\frac{1}{n}}(c) [SI](c) e^{\tau c} e^{-\tau u} [S]^{\frac{n-1}{n}}(u) dc \\ &\quad - \int_0^u \int_0^c \tau \kappa [S]^{-\frac{1}{n}}(c-a) [SI](c-a) f(a) e^{-\tau a} e^{\tau c} e^{-\tau u} [S]^{\frac{n-1}{n}}(u) da dc \\ &\quad - \int_0^u \int_c^\infty \frac{n}{N} [S]_0^{\frac{1}{n}} \varphi(a-c) \frac{f(a)}{\xi(a-c)} e^{-\tau u} [S]^{\frac{n-1}{n}}(u) da dc. \end{aligned}$$

Then, substituting this formula into the first equation of (3.2), we find an equation in general form

$$[S]'(t) = -\tau A(t) [S]^{\frac{n-1}{n}}(t), \quad (3.20)$$

where

$$\begin{aligned} A(u) &= \frac{[SI](0)}{[S]^{\frac{n-1}{n}}(0)} e^{-\tau u} + \int_0^u \tau \kappa [S]^{-\frac{1}{n}}(c) [SI](c) e^{\tau c} e^{-\tau u} dc \\ &\quad - \int_0^u \int_0^c \tau \kappa [S]^{-\frac{1}{n}}(c-a) [SI](c-a) f(a) e^{-\tau a} e^{\tau c} e^{-\tau u} da dc \\ &\quad - \int_0^u \int_c^\infty \frac{n}{N} [S]_0^{\frac{1}{n}} \varphi(a-c) \frac{f(a)}{\xi(a-c)} e^{-\tau u} da dc. \end{aligned} \quad (3.21)$$

Solving this scalar equation, we have

$$[S]^{\frac{1}{n}}(t) = [S]_0^{\frac{1}{n}} - \frac{\tau}{n} \int_0^t A(u) du.$$

For the final size relation, we consider the following equation

$$[S]_\infty^{\frac{1}{n}} = [S]_0^{\frac{1}{n}} - \frac{\tau}{n} \int_0^\infty A(u) du. \quad (3.22)$$

Using the linearity of integration, we have to calculate the following four integrals on the right-hand side:

$$\begin{aligned} I_1 &= \int_0^\infty \frac{[SI](0)}{[S]^{\frac{n-1}{n}}(0)} e^{-\tau u} du, \\ I_2 &= \int_0^\infty \int_0^u \tau \kappa [S]^{-\frac{1}{n}}(c) [SI](c) e^{\tau c} e^{-\tau u} dc du, \\ I_3 &= \int_0^\infty \int_0^u \int_0^c \tau \kappa [S]^{-\frac{1}{n}}(c-a) [SI](c-a) f(a) e^{-\tau a} e^{\tau c} e^{-\tau u} dadcdu, \\ I_4 &= \int_0^\infty \int_0^u \int_c^\infty \frac{n}{N} [S]_0^{\frac{1}{n}} \varphi(a-c) \frac{f(a)}{\xi(a-c)} e^{-\tau u} da dc du. \end{aligned}$$

After lengthy calculations (see Appendix (c)), we arrive to the relation

$$[S]_\infty^{\frac{1}{n}} = [S]_0^{\frac{1}{n}} + \kappa \frac{1}{n-1} \left(1 - \int_0^\infty f(a) e^{-\tau a} da \right) \left([S]_\infty^{\frac{n-1}{n}} - [S]_0^{\frac{n-1}{n}} \right). \quad (3.23)$$

After some algebraic manipulation and substituting back the formula of κ , we have

$$\frac{s_{\infty}^{\frac{1}{n}} - 1}{\frac{1}{n-1}} = \frac{n-1}{N} (1 - \mathcal{L}[f](\tau)) [S]_0 \left(s_{\infty}^{\frac{n-1}{n}} - 1 \right), \quad (3.24)$$

where $\mathcal{L}[f](\tau)$ denotes the Laplace transform of f , the PDF of recovery time at τ . \square

Notice that for $n \rightarrow \infty$, the relation (3.18) takes the form $\ln(s_{\infty}) = \mathcal{R}_0^p(s_{\infty} - 1)$, which is exactly the classical form of final size relations. Furthermore, simple algebraic manipulations show that our final size relation (3.24) agrees with that derived in [10].

4. Special cases

In this section, we investigate some common choices for the recovery time. As we expect, if $\mathcal{I} \sim \text{Exp}(\gamma)$ (i.e. the infectious period \mathcal{I} is exponentially distributed), we get back the classical Markovian models. In the case of fixed recovery time, the models reduce to the systems studied in detail in [19]. We can also recover the multi-stage infection model of [36] with gamma distributed recovery time. Finally, we consider $\mathcal{I} \sim \text{Uniform}(A, B)$ and write down the associated equations in a compact form. In this section we assume, that the initial infecteds are 'newborn', i.e. the initial distribution of infected nodes $\varphi(a) = [I]_0 \delta(a)$, where $\delta(a)$ is the Dirac delta function. Then,

$$\int_t^{\infty} \varphi(a-t) \frac{f(a)}{\xi(a-t)} da = [I]_0 f(t) \quad (4.1)$$

and

$$\int_t^{\infty} \frac{n}{N} [S]_0 \varphi(a-t) e^{-\int_0^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} \frac{f(a)}{\xi(a-t)} da = \frac{n}{N} [S]_0 e^{-\int_0^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} f(t). \quad (4.2)$$

(a) Exponential distribution with parameter γ

The most widely used distribution in disease modelling is the exponential distribution. Both the stochastic and deterministic approaches exploit the memorylessness property to build tractable models. The resulting deterministic systems are ordinary differential equations, which are favoured due to their simpler structure and numerical solvability. In the exponential case, $\xi(t) = e^{-\gamma t}$ and $f(t) = \gamma e^{-\gamma t}$. Using the assumption $\varphi(a) = [I]_0 \delta(a)$, (3.3) and $f(t) = \gamma \xi(t)$, from (2.6c) we obtain

$$[\dot{I}](t) = \tau [SI](t) - \gamma [I](t),$$

which gives the classical Markovian type pairwise equation for $[I](t)$. With similar arguments, from (2.6d) we obtain

$$\begin{aligned} [\dot{SI}](t) &= \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)} [SI](t) - \tau [SI](t) \\ &\quad - \gamma [SI](t). \end{aligned}$$

For the mean-field model (2.8), the same calculation gives the classical Markovian mean-field equation for $\dot{I}(t)$:

$$[\dot{I}](t) = \tau S(t)I(t) - \gamma I(t).$$

(b) Fixed recovery time σ

In several models, it is a reasonable assumption for the infectious period to have a fixed, constant duration, e.g. for measles [1]. In the case of fixed recovery time σ , we have

$$\xi(t) = \begin{cases} 1 & \text{if } 0 \leq t < \sigma, \\ 0 & \text{if } t \geq \sigma, \end{cases}$$

and

$$f(t) = \delta(t - \sigma),$$

where $\delta(t)$ denotes the Dirac-delta function. Applying the fundamental property of $\delta(t)$, from (2.6c) and $\varphi(a) = [I]_0 \delta(a)$ we have

$$[\dot{I}](t) = \tau[SI](t) - \begin{cases} 0 & \text{if } 0 \leq t < \sigma, \\ \tau[SI](t - \sigma) & \text{if } t \geq \sigma, \end{cases}$$

and from (2.6d), if $0 \leq t < \sigma$, we obtain

$$[\dot{S}I](t) = \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)} [SI](t) - \tau[SI](t).$$

If $t > \sigma$, we get

$$\begin{aligned} [\dot{S}I](t) &= \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)} [SI](t) - \tau[SI](t) \\ &\quad - \tau \frac{n-1}{n} \frac{[SS](t-\sigma)[SI](t-\sigma)}{[S](t-\sigma)} e^{-\int_{t-\sigma}^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds}. \end{aligned}$$

which is exactly the same system, that was studied in detail in [19]. The mean-field model for fixed recovery time (see [19]) can also be derived from (2.8b) using the same arguments.

(c) Gamma distribution with shape $K \in \mathbb{Z}^+$ and rate $K\gamma$

The case of gamma distributed recovery time was studied in [36].

Using pairwise approximation with a standard closure, the authors have been able to analytically derive a number of important characteristics of disease dynamics. These included the final size of an epidemic and the epidemic threshold. Their results have shown that a higher number of disease stages, but with the same average duration of the infectious period, results in faster epidemic outbreaks with a higher peak prevalence and a larger final size of the epidemic. The pairwise model in [36] has the following equations for nodes:

$$\begin{aligned} [\dot{S}] &= -\tau \sum_{i=1}^K [SI_i], \\ [\dot{I}_1] &= \tau \sum_{i=1}^K [SI_i] - K\gamma[I_1] \\ [\dot{I}_j] &= K\gamma[I_{j-1}] - K\gamma[I_j], \quad j = 2, 3, \dots, K, \end{aligned} \tag{4.3}$$

where I_i , $i = 1, 2, \dots, K$ are the infectious stages, where nodes spend an exponentially distributed time with parameter $K\gamma$. The distribution of the total infectious period is the sum of K exponential distributions with parameter $K\gamma$, which gives the gamma distribution with shape K and rate $K\gamma$ (thus the expected infectious period is $K \times 1/K\gamma = 1/\gamma$). Clearly, $[I](t) =$

$\sum_{j=1}^K [I_j](t)$ and $[SI](t) = \sum_{i=1}^K [SI_i](t)$ and the sum of equations for infectious stages gives

$$[\dot{I}](t) = \tau[SI](t) - K\gamma[I_K](t).$$

On the other hand, using (4.1), the PDF and survival function of Gamma distribution

$$\begin{aligned} f(a) &= \frac{(K\gamma)^K}{(K-1)!} a^{K-1} e^{-K\gamma a}, \\ \xi(a) &= e^{-K\gamma a} \sum_{k=0}^{K-1} \frac{(K\gamma)^k}{k!} a^k, \end{aligned}$$

and inserting into (2.6c) and (3.3), we have

$$[\dot{I}](t) = \tau[SI](t) - K\gamma \left(\int_0^t \tau[SI](t-a) \frac{(K\gamma)^{K-1}}{(K-1)!} a^{K-1} e^{-K\gamma a} da - [I]_0 \frac{(K\gamma)^{K-1}}{(K-1)!} t^{K-1} e^{-K\gamma t} \right) \quad (4.4)$$

and

$$[I](t) = \sum_{k=0}^{K-1} \left(\int_0^t \tau[SI](t-a) \frac{(K\gamma)^k}{k!} a^k e^{-K\gamma a} da - [I]_0 \frac{(K\gamma)^k}{k!} t^k e^{-K\gamma t} \right). \quad (4.5)$$

These equations suggest the relations

$$[I_j](t) = \int_0^t \tau[SI](t-a) \frac{(K\gamma)^{j-1}}{(j-1)!} a^{j-1} e^{-K\gamma a} da + [I]_0 \frac{(K\gamma)^{j-1}}{(j-1)!} t^{j-1} e^{-K\gamma t}, \quad j = 1, 2, \dots, K. \quad (4.6)$$

To show this, we consider the equations for infectious stages in (4.3) as a first-order, linear differential equations with variation of constants formulae

$$[I_1](t) = [I_1](0)e^{-K\gamma t} + \int_0^t e^{-K\gamma(t-s)} \tau[SI](s) ds \quad (4.7)$$

and

$$[I_j](t) = [I_j](0)e^{-K\gamma t} + \int_0^t e^{-K\gamma(t-s)} K\gamma [I_{j-1}](s) ds, \quad j = 2, 3, \dots, K. \quad (4.8)$$

If all infecteds are newborn, we have $[I_1](0) = [I]_0$ and $[I_2](0) = [I_3](0) = \dots = [I_K](0) = 0$. Proceeding by induction yields that (4.6) satisfies (4.7) for $j = 1$ and (4.8) for $j = 2, 3, \dots, K$ (for details, see Appendix (d)). It is analogous to derive the equations for $[SI_j](t)$.

(d) Uniform distribution on interval $[A, B]$

The uniform distribution is one of the most natural probability distributions and preferred in agent-based modeling [20], and was applied also for avian influenza [47]. Let the recovery time be distributed uniformly on interval $[A, B]$ (we assume $0 < A < B$), i.e.

$$f(t) = \begin{cases} \frac{1}{B-A} & \text{if } t \in (A, B), \\ 0 & \text{otherwise,} \end{cases}$$

and

$$\xi(t) = \begin{cases} 1 & \text{if } t \leq A, \\ \frac{B-t}{B-A} & \text{if } t \in (A, B), \\ 0 & \text{if } t \geq B. \end{cases}$$

We have to study the three cases $t < A$, $A < t < B$ and $t > B$. Writing the equation for $[\dot{I}](t)$, we have (after changing the variable):

$$[\dot{I}](t) = \tau[SI](t) - \begin{cases} 0 & \text{if } t < A, \\ \int_0^{t-A} \frac{\tau[SI](u)}{B-A} du + \frac{[I]_0}{B-A} & \text{if } t \in [A, B], \\ \int_{t-B}^{t-A} \frac{\tau[SI](u)}{B-A} du & \text{if } t > B. \end{cases}$$

With a more compact notation,

$$[\dot{I}](t) = \tau[SI](t) - \int_{\max(0, t-B)}^{\max(0, t-A)} \frac{\tau[SI](u)}{B-A} du - \frac{[I]_0}{B-A} \chi_{[A, B]}(t),$$

where $\chi_{[A, B]}(t)$ is the indicator function of interval $[A, B]$. The same argument gives

$$\begin{aligned} [\dot{S}I](t) &= \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)} [SI](t) - \tau[SI](t) \\ &\quad - \int_{\max(0, t-B)}^{\max(0, t-A)} \frac{\tau}{B-A} \frac{n-1}{n} \frac{[SS](u)[SI](u)}{[S](u)} e^{-\int_u^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} du \\ &\quad - \frac{n}{N} [S]_0 e^{-\int_0^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} \frac{[I]_0}{B-A} \chi_{[A, B]}(t). \end{aligned}$$

For $t > B$ the model becomes a system of differential equations with distributed delays.

5. Discussion

While the main focus of this paper is on the derivation and rigorous analysis of the model, we have performed a number of numerical tests where the results of explicit stochastic network simulations on networks are compared to the output from the generalised pairwise model. In Fig. 1(a), regular random networks were considered and the average of 100 simulations is compared to the numerical solutions of mean-field (2.7) and pairwise (2.6) models. Several observations can be made: (a) the agreement of the simulation results with the numerical solution of pairwise model is excellent, and (b) the mean-field model, which largely ignores the network structure, performs poorly. We note that distributions with the same mean but smaller variance lead to epidemics that grow faster initially (see also [34] and [2]). We emphasise that a key strength of our model is to approximate the whole time course of the epidemic. Furthermore, in Fig. 1(b,c) we test if the analytical threshold (3.9) and final epidemic size formula (3.24) are accurate when compared to simulations. These clearly demonstrate that our analytical results agree with simulations and this gives us great confidence that the generalised pairwise model can and will be used in different contexts as dictated by empirical or other theoretical studies.

The generalised model is more challenging to analyse due to its complexity, but it largely relies on tools from the theory of integro-differential equations. Further extensions of the model could focus on relaxing the assumption of regular networks and extend the model to networks with heterogeneous degree distribution, see for example [37,39], or to consider modelling the situation where both the infectious and recovery processes are non-Markovian.

Our pairwise model is developed for regular networks where each node has the same number of links. It is well-known that such ODE-based models will also provide good approximations if epidemics are considered on Erdős-Rényi networks with the same mean, due to the efficient mixing within the network. It will however fail to provide good agreement for networks with highly heterogeneous degrees even if the mean is the same. Our proposed model, as most pairwise models and models based on the message passing approach and edge-based compartmental models, are primarily designed for Configuration Model networks, and thus with clustering going to zero in the limit of large networks. Extending any of these to clustered networks is still a major challenge and has so far been only done when clustering is introduced in a very specific way, e.g., non-overlapping triangles or other clustering inducing subgraphs or motifs,

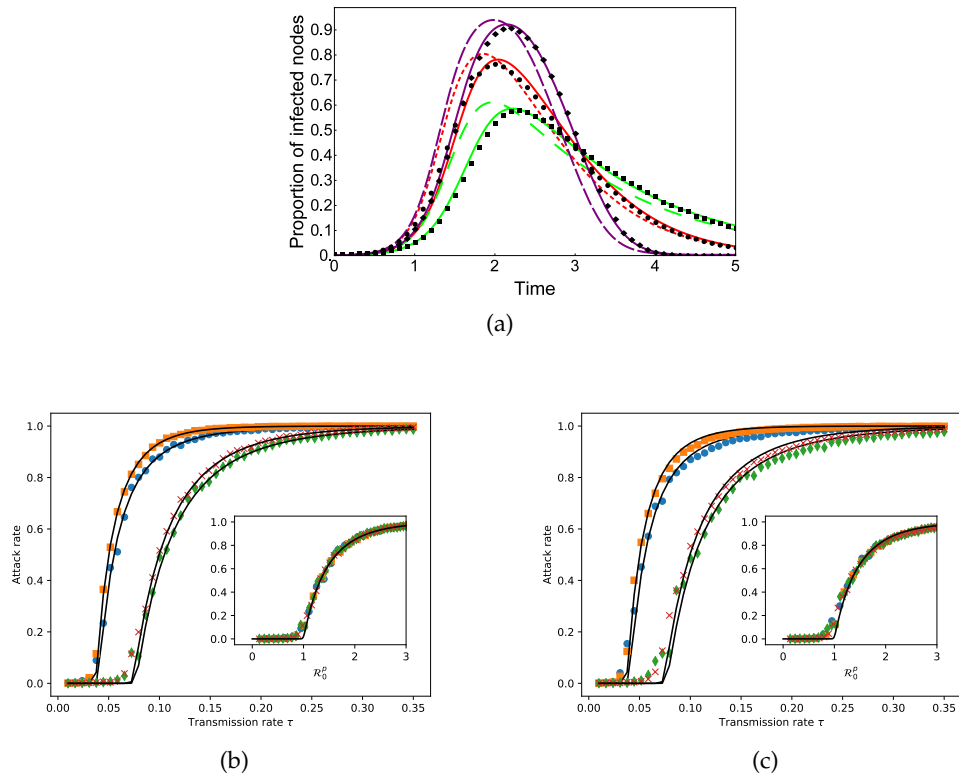


Figure 1: (a) Stochastic and numerical experiments for non-Markovian epidemic with various recovery time distributions on regular networks with $N = 1000$ nodes and infection rate $\tau = 0.35$. Squares, circles, diamonds show the mean of 100 simulations on regular graphs with $k = 15$ for exponential distribution with rate $2/3$ (mean $= 3/2$, variance $= 9/4$), gamma distribution with shape $\alpha = 3$ and rate $\beta = 2$ (mean $= 3/2$, variance $= 3/4$), uniform distribution on interval $[a, b] = [1, 2]$ (mean $= 3/2$, variance $= 1/2$), respectively. Simulations started with a single newly infected node and a matching initial condition was considered for the integro-differential system. Dashed and solid lines correspond to the numerical solution of the mean-field (2.7) and pairwise (2.6) models, respectively. Attack rate based on explicit stochastic network simulations is plotted against τ and \mathcal{R}_0^p (in the inset) for regular (b) and Erdős-Rényi networks (c) with $\langle k \rangle = 15$, the theoretical curves (continuous black lines) are based on (3.24). The circle, diamond, square and cross stand for gamma (shape $\alpha = 0.5$, $\beta = 0.25$ with mean $= 2$, variance $= 8$), uniform (on $[a, b] = [1, 3]$ with mean $= 2$, variance $= 1/3$), exponential (with rate 1 and mean $= 1$, variance $= 1$) and Dirac delta distributions (fixed at 1 with mean $= 1$, variance $= 0$). For (b) and (c), $N = 10000$ and results are based on averaging over 1000 simulations where each epidemic starts with exactly one infectious node. The error bars are smaller than the markers and thus not plotted.

see [26,44]. Pairwise models for Markovian epidemics and for infectious periods of a fixed length can be extended to heterogeneous networks, at the cost of a much larger number of equations. Thus our general model may require us to start with a system of PDEs with many equations to capture degree heterogeneity. We foresee that while this may be possible, it would probably involve highly complex and technical calculations. Potentially a more natural extension of our model would be to relax the assumption of Markovian transmission, and this is indeed a more promising future research direction. We note that Wilkinson et al. [46] have independently derived a similar pairwise model by starting from the message passing system [13], assuming

that the initial distribution of infected nodes is $\xi(a) = [I]_0 \delta(a)$. However, our model can handle arbitrary initial conditions.

Several different approaches exist to model non-Markovian epidemics on networks. These are largely guided by the choice of model and variables to be tracked. Notable examples include the message passing approach, often referred to as the cavity model [13,45], the edge based compartmental model [38] which has recently been generalised to arbitrary infection and recovery processes, and the percolation based approach [17,24,27,28]. While the latter only offers information about the final state of the epidemic, the former two describes the temporal evolution of the epidemic. Generalisations of the pairwise model to gamma-distributed infectious periods have also been proposed and this has been developed for both homogeneous and heterogeneous networks [36,37]. As for Markovian epidemics, we expect that many of the models mentioned above are complementary and offer different perspectives on the time evolution or final state of the epidemic. We expect that many of the non-Markovian models will in fact be equivalent under appropriately chosen initial conditions and appropriate averaging. With the model we proposed in this paper, we wanted to emphasise opportunities to frame models of epidemics on networks in more rigorous mathematical terms and use existing mathematical theory to enhance our understanding of stochastic processes on networks and their average behaviour as captured by mean-field models.

A. Appendix

(a) Calculations for model derivation

Repeating Eq. (2.1a) and applying the moment-closure formula (2.4) to Eq. (2.1c), we have

$$\begin{aligned} [\dot{S}](t) &= -\tau[SI](t), \\ [\dot{SI}](t) &= -2\tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)}. \end{aligned}$$

Using $[I](t) = \int_0^\infty i(t, a) da$, from Eq. (2.1b) we obtain

$$\begin{aligned} [\dot{I}](t) &= \int_0^\infty \frac{\partial}{\partial t} i(t, b) db = \int_0^\infty \left(-h(b)i(t, b) - \frac{\partial}{\partial b} i(t, b) \right) db \\ &= - \int_0^\infty h(b)i(t, b) db - (i(t, \infty) - i(t, 0)) = - \int_0^\infty h(b)i(t, b) db - i(t, \infty) + i(t, 0). \end{aligned} \quad (\text{A } 1)$$

Solving the first-order linear PDE (2.1b) along characteristic lines, we obtain

$$i(t, a) = \begin{cases} i(t-a, 0)e^{-\int_0^a h(b)db}, & \text{if } t > a; \\ i(0, a-t)e^{-\int_{a-t}^a h(b)db}, & \text{if } t \leq a. \end{cases}$$

Plugging (2.2a) and (2.3a) into the solution above, we have

$$i(t, a) = \begin{cases} \tau[SI](t-a)e^{-\int_0^a h(b)db}, & \text{if } t > a; \\ \varphi(a-t)e^{-\int_{a-t}^a h(b)db}, & \text{if } t \leq a. \end{cases} \quad (\text{A } 2)$$

Applying this formula for $[I](t) = \int_0^\infty i(t, a) da$, we find

$$[I](t) = \int_0^t \tau[SI](t-a)e^{-\int_0^a h(b)db} da + \int_t^\infty \varphi(a-t)e^{-\int_{a-t}^a h(b)db} da. \quad (\text{A } 3)$$

Finally, using that along the characteristic lines, $i(t, \infty) = i(0, \infty) = \varphi(\infty) = 0$ from the assumption, substituting (A 2) and the boundary condition (2.2a) into (A 1), we get

$$\begin{aligned} [\dot{I}](t) &= \tau[SI](t) - \int_0^t \tau[SI](t-a)h(a)e^{-\int_0^a h(b)db} da \\ &\quad - \int_t^\infty \varphi(a-t)h(a)e^{-\int_{a-t}^a h(b)db} da. \end{aligned} \quad (\text{A } 4)$$

Using the definition and properties of hazard function, we can deduce the following formulae:

$$e^{-\int_0^a h(b)db} = \frac{\xi(a)}{\xi(0)} = \xi(a), \quad (\text{A } 5a)$$

$$e^{-\int_{a-t}^a h(b)db} = \frac{\xi(a)}{\xi(a-t)}, \quad (\text{A } 5b)$$

$$h(a)e^{-\int_0^a h(b)db} = f(a), \quad (\text{A } 5c)$$

$$h(a)e^{-\int_{a-t}^a h(b)db} = \frac{f(a)}{\xi(a-t)}. \quad (\text{A } 5d)$$

Applying these formulae to Eqs. (A 3) and (A 4), we have

$$[I](t) = \int_0^t \tau[SI](t-a)\xi(a)da + \int_t^\infty \varphi(a-t)\frac{\xi(a)}{\xi(a-t)} da, \quad (\text{A } 6)$$

and

$$[\dot{I}](t) = \tau[SI](t) - \int_0^t \tau[SI](t-a)f(a)da - \int_t^\infty \varphi(a-t)\frac{f(a)}{\xi(a-t)} da.$$

To compute the equation for $[SI](t)$, we follow the calculation process above. First, applying (2.5) to Eq. (2.1d), we get

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) Si(t, a) = -\frac{\tau(n-1)}{n} \frac{[SI](t)}{[S](t)} Si(t, a) - (\tau + h(a))Si(t, a). \quad (\text{A } 7)$$

Using $[SI](t) = \int_0^\infty Si(t, a)da$, from Eq. (A 7) we find

$$\begin{aligned} [\dot{SI}](t) &= \int_0^\infty \frac{\partial}{\partial t} Si(t, a)da \\ &= \int_0^\infty \left(-\frac{\tau(n-1)}{n} \frac{[SI](t)}{[S](t)} Si(t, a) \right) da - \int_0^\infty (\tau + h(a))Si(t, a)da - \int_0^\infty \frac{\partial}{\partial a} Si(t, a)da \\ &= -\tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)} [SI](t) - \tau[SI](t) - \int_0^\infty h(a)Si(t, a)da - Si(t, \infty) + Si(t, 0). \end{aligned} \quad (\text{A } 8)$$

We want to express the variable $Si(t, a)$ as a function of classical network variables. To achieve this, let us consider the following first-order PDE:

$$\left(\frac{\partial}{\partial t} + \frac{\partial}{\partial a} \right) x(t, a) = -f(t)x(t, a) - g(a)x(t, a)$$

with boundary conditions

$$x(t, 0) = \phi(t), \quad x(0, a) = \psi(a).$$

Solving along the characteristic lines $t - a = c$, we find that

$$x(t, a) = \begin{cases} \phi(t-a)e^{-\int_{t-a}^t f(s)ds} e^{-\int_0^a g(b)db}, & \text{if } t > a; \\ \psi(a-t)e^{-\int_0^t f(s)ds} e^{-\int_{a-t}^a g(b)db}, & \text{if } t \leq a. \end{cases} \quad (\text{A } 9)$$

In our case, $x(t, a) = Si(t, a)$, $f(t) = \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)}$, $g(a) = \tau + h(a)$, $\phi(t) = \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)}$, (from closure approximation (2.5)) and $\psi(a) = \frac{n}{N} [S]_0 \varphi(a)$, hence from (A 9) we get

$$Si(t, a) = \begin{cases} \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} e^{-\int_{t-a}^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} ds} e^{-\int_0^a \tau + h(b) db}, & \text{if } t > a; \\ \frac{n}{N} [S]_0 \varphi(a-t) e^{-\int_0^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} ds} e^{-\int_{a-t}^a \tau + h(b) db}, & \text{if } t \leq a. \end{cases} \quad (\text{A } 10)$$

Again, along the characteristic lines $Si(t, \infty) = Si(0, \infty) = \chi(\infty) = 0$. Putting (A 10) into $[SI](t) = \int_0^\infty Si(t, a) da$, we obtain

$$\begin{aligned} [SI](t) &= \int_0^t \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} e^{-\int_{t-a}^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} ds} e^{-\int_0^a \tau + h(b) db} da \\ &\quad + \int_t^\infty \frac{n}{N} [S]_0 \varphi(a-t) e^{-\int_0^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} ds} e^{-\int_{a-t}^a \tau + h(b) db} da. \end{aligned} \quad (\text{A } 11)$$

If we substitute (A 10) back into Eq. (A 8), we obtain

$$\begin{aligned} [\dot{SI}](t) &= \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \frac{\tau(n-1)}{n} \frac{[SI](t)}{[S](t)} [SI](t) - \tau [SI](t) \\ &\quad - \int_0^t \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} e^{-\int_{t-a}^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} ds} e^{-\int_0^a \tau + h(b) db} h(a) da \\ &\quad - \int_t^\infty \frac{n}{N} [S]_0 \varphi(a-t) e^{-\int_0^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} ds} e^{-\int_{a-t}^a \tau + h(b) db} h(a) da. \end{aligned} \quad (\text{A } 12)$$

Applying the formulae (A 5a)-(A 5d) in Eqs. (A 11) and (A 12), we have

$$\begin{aligned} [SI](t) &= \int_0^t \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} e^{-\int_{t-a}^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} \xi(a) da \\ &\quad + \int_t^\infty \frac{n}{N} [S]_0 \varphi(a-t) e^{-\int_0^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} \frac{\xi(a)}{\xi(a-t)} da, \end{aligned} \quad (\text{A } 13)$$

and

$$\begin{aligned} [\dot{SI}](t) &= \tau \frac{n-1}{n} \frac{[SS](t)[SI](t)}{[S](t)} - \tau \frac{n-1}{n} \frac{[SI](t)}{[S](t)} [SI](t) - \tau [SI](t) \\ &\quad - \int_0^t \tau \frac{n-1}{n} \frac{[SS](t-a)[SI](t-a)}{[S](t-a)} e^{-\int_{t-a}^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} f(a) da \\ &\quad - \int_t^\infty \frac{n}{N} [S]_0 \varphi(a-t) e^{-\int_0^t \tau \frac{n-1}{n} \frac{[SI](s)}{[S](s)} + \tau ds} \frac{f(a)}{\xi(a-t)} da. \end{aligned}$$

(b) Calculation for final size relation (3.13)

In this section, we show the steps of going from (3.16) to (3.17):

$$\begin{aligned} \ln \left(\frac{S(\infty)}{S(0)} \right) &= - \left(\tau \frac{n}{N} \right)^2 \int_0^\infty \int_0^u S(u-a) I(u-a) \xi(a) da du \\ &= - \left(\tau \frac{n}{N} \right)^2 \int_0^\infty \int_0^u S(v) I(v) \xi(u-v) dv du = - \left(\tau \frac{n}{N} \right)^2 \int_0^\infty \int_v^\infty S(v) I(v) \xi(u-v) du dv \\ &= - \left(\tau \frac{n}{N} \right)^2 \int_0^\infty S(v) I(v) \left[\int_v^\infty \xi(u-v) du \right] dv = - \left(\tau \frac{n}{N} \right)^2 \int_0^\infty S(v) I(v) \left[\int_0^\infty \xi(p) dp \right] dv \\ &= \tau \frac{n}{N} \left[\int_0^\infty \xi(p) dp \right] (S(\infty) - S(0)) = \tau \frac{n}{N} \left[\int_0^\infty \int_p^\infty f(q) dq dp \right] (S(\infty) - S(0)) \\ &= \tau \frac{n}{N} \left[\int_0^\infty \int_0^q f(q) dp dq \right] (S(\infty) - S(0)) = \tau \frac{n}{N} \left[\int_0^\infty q f(q) dq \right] (S(\infty) - S(0)) \\ &= \tau \frac{n}{N} \mathbb{E}(\mathcal{I}) (S(\infty) - S(0)). \end{aligned}$$

(c) Calculation for final size relation (3.18)

We compute the integrals appear on the right-hand side of Eq. (3.22). For the first one, we have

$$I_1 = \int_0^\infty \frac{[SI](0)}{[S]^{\frac{n-1}{n}}(0)} e^{-\tau u} du = \frac{[SI](0)}{[S]^{\frac{n-1}{n}}(0)} \left[\frac{e^{-\tau u}}{-\tau} \right]_0^\infty = \frac{[SI](0)}{[S]^{\frac{n-1}{n}}(0)} \frac{1}{\tau}.$$

After some algebraic manipulation, we obtain the following expression for the second integral I_2 :

$$\begin{aligned} I_2 &= \int_0^\infty \int_0^u \tau \kappa [S]^{-\frac{1}{n}}(c) [SI](c) e^{\tau c} e^{-\tau u} dc du = \int_0^\infty \int_c^\infty \tau \kappa [S]^{-\frac{1}{n}}(c) [SI](c) e^{\tau c} e^{-\tau u} du dc \\ &= \int_0^\infty \tau \kappa [S]^{-\frac{1}{n}}(c) [SI](c) e^{\tau c} \left[\frac{e^{-\tau u}}{-\tau} \right]_c^\infty dc = \int_0^\infty \tau \kappa [S]^{-\frac{1}{n}}(c) [SI](c) e^{\tau c} \frac{e^{-\tau c}}{\tau} dc \\ &= -\frac{1}{\tau} \kappa \int_0^\infty [S]^{-\frac{1}{n}}(c) [\dot{S}](c) dc = -\frac{1}{\tau} \kappa \frac{n}{n-1} \left([S]_\infty^{\frac{n-1}{n}} - [S]_0^{\frac{n-1}{n}} \right). \end{aligned}$$

The most challenging one is the third integral I_3 :

$$\begin{aligned} I_3 &= \int_0^\infty \int_0^u \int_0^c \tau \kappa [S]^{-\frac{1}{n}}(c-a) [SI](c-a) f(a) e^{-\tau a} e^{\tau c} e^{-\tau u} da dc du \\ &= \int_0^\infty \int_c^\infty \int_0^c \tau \kappa [S]^{-\frac{1}{n}}(c-a) [SI](c-a) f(a) e^{-\tau a} e^{\tau c} e^{-\tau u} du da dc \\ &= \int_0^\infty \int_0^c \int_c^\infty \tau \kappa [S]^{-\frac{1}{n}}(c-a) [SI](c-a) f(a) e^{-\tau a} e^{\tau c} e^{-\tau u} du da dc \\ &= \int_0^\infty \int_0^c \tau \kappa [S]^{-\frac{1}{n}}(c-a) [SI](c-a) f(a) e^{-\tau a} e^{\tau c} \left[\frac{e^{-\tau u}}{-\tau} \right]_c^\infty da dc \\ &= \frac{1}{\tau} \int_0^\infty \int_0^c \tau \kappa [S]^{-\frac{1}{n}}(c-a) [SI](c-a) f(a) e^{-\tau a} da dc \\ &= -\frac{1}{\tau} \kappa \int_0^\infty f(a) e^{-\tau a} \left[\frac{[S]^{\frac{n-1}{n}}(c-a)}{\frac{n-1}{n}} \right]_a^\infty da \\ &= -\frac{1}{\tau} \kappa \frac{n}{n-1} \left([S]_\infty^{\frac{n-1}{n}} - [S]_0^{\frac{n-1}{n}} \right) \int_0^\infty f(a) e^{-\tau a} da. \end{aligned}$$

For the fourth integral, we get

$$\begin{aligned} I_4 &= \int_0^\infty \int_0^u \int_c^\infty \frac{n}{N} [S]_0^{\frac{1}{n}} \varphi(a-c) \frac{f(a)}{\xi(a-c)} e^{-\tau u} da dc du \\ &= \int_0^\infty \int_c^\infty \int_c^\infty \frac{n}{N} [S]_0^{\frac{1}{n}} \varphi(a-c) \frac{f(a)}{\xi(a-c)} e^{-\tau u} du da dc \\ &= \int_0^\infty \int_c^\infty \int_c^\infty \frac{n}{N} [S]_0^{\frac{1}{n}} \varphi(a-c) \frac{f(a)}{\xi(a-c)} e^{-\tau u} du da dc \\ &= \int_0^\infty \int_c^\infty \frac{n}{N} [S]_0^{\frac{1}{n}} \varphi(a-c) \frac{f(a)}{\xi(a-c)} \left[\frac{e^{-\tau u}}{-\tau} \right]_c^\infty da dc \\ &= \frac{1}{\tau} \int_0^\infty \int_c^\infty \frac{n}{N} [S]_0^{\frac{1}{n}} \varphi(a-c) \frac{f(a)}{\xi(a-c)} e^{-\tau c} da dc. \end{aligned}$$

Having a small amount of initial infecteds (i.e. $[I](0) = \int_0^\infty \varphi(a) da \ll 1$), the integrals I_1 and I_4 are approximately zero.

(d) Calculations for proof of equivalence in the case of gamma distribution

Here, we obtain the formula (4.6) by induction from variation of constants formulae (4.7) and (4.8). Letting $j = 1$ in (4.6), we have

$$[I_1](t) = \int_0^t \tau[SI](t-a)e^{-K\gamma a} da + [I]_0 e^{-K\gamma t},$$

which comes directly from (4.7). Assuming that (4.6) holds for $1 < j$, we prove that it holds for $j + 1$. Indeed, we can do the following elaboration:

$$\begin{aligned} [I_{j+1}](t) &= [I_{j+1}](0)e^{-K\gamma t} + \int_0^t e^{-K\gamma(t-s)} K\gamma[I_j](s) ds \\ &= \int_0^t e^{-K\gamma(t-s)} K\gamma \left(\int_0^s \tau[SI](s-a) \frac{(K\gamma)^{j-1}}{(j-1)!} a^{j-1} e^{-K\gamma a} da + [I]_0 \frac{(K\gamma)^{j-1}}{(j-1)!} s^{j-1} e^{-K\gamma s} \right) ds \\ &= \int_0^t \frac{(K\gamma)^j}{(j-1)!} e^{-K\gamma(t-s)} \left(\int_0^s \tau[SI](s-a) a^{j-1} e^{-K\gamma a} da ds \right) + [I]_0 \frac{(K\gamma)^j}{(j-1)!} e^{-K\gamma t} \int_0^t s^{j-1} ds \\ &= \int_0^t \frac{(K\gamma)^j}{(j-1)!} e^{-K\gamma(t-s)} \left(\int_0^s \tau[SI](u)(s-u)^{j-1} e^{-K\gamma(s-u)} du \right) ds + [I]_0 \frac{(K\gamma)^j}{j!} t^j e^{-K\gamma t} \\ &= \int_0^t \frac{(K\gamma)^j}{(j-1)!} e^{-K\gamma(t-u)} \tau[SI](u) \left(\int_u^t (s-u)^{j-1} ds \right) du + [I]_0 \frac{(K\gamma)^j}{j!} t^j e^{-K\gamma t} \\ &= \int_0^t \tau[SI](u) \frac{(K\gamma)^j}{j!} (t-u)^j e^{-K\gamma(t-u)} du + [I]_0 \frac{(K\gamma)^j}{j!} t^j e^{-K\gamma t} \\ &= \int_0^t \tau[SI](t-a) \frac{(K\gamma)^j}{j!} a^j e^{-K\gamma a} da + [I]_0 \frac{(K\gamma)^j}{j!} t^j e^{-K\gamma t}. \end{aligned}$$

(e) Implementation of numerical simulations

As a validation of our models, we implemented an event-based stochastic algorithm for simulating the non-Markovian SIR process with arbitrary recovery time. In the code, the waiting times for possible events are generated from appropriate distributions. After selecting the smallest waiting time, the associated event (infection or recovery) happens, and according to the type of event, the necessary updates are executed.

For the numerical solution of integro-differential equations (2.6) and (2.7), we developed a numerical scheme based on collocation method. The numerical methods in [7] were adapted to the reduced, but highly nonlinear pairwise system, having the following general form:

$$\begin{aligned} x'(t) &= f(x(t), y(t)), \\ y'(t) &= g(x(t), y(t)) - \int_0^t F(t-a, x(a), y(a)) e^{-\int_a^t G(x(s), y(s)) ds} da \\ &\quad - H\left(t, \int_0^t G(x(s), y(s)) ds\right). \end{aligned} \quad (\text{A } 14)$$

A collocation solution u_h to a functional equation on an interval I is an element from some finite-dimensional function space (the collocation space) which satisfies the equation on an appropriate finite subset of points in I (the set of collocation points), whose cardinality essentially matches the dimension of the collocation space. For integro-differential equations the collocation equations are not yet in a form amenable to numerical computation, due to the presence of the memory term given by the integral operator, thus another discretisation step, based on appropriate quadrature approximations, is necessary to obtain the fully discretised collocation scheme. The presence of the double integral in (A 14) makes our scheme different from standard methods.

Data Accessibility. This paper has no data.

Competing Interests. We have no competing interests.

Authors' Contributions. GR and IK conceived the study. GR and ZV derived the model and performed mathematical analysis. ZV and IK performed stochastic and numerical analysis, and put the research into the context of network theory. All authors contributed to writing the manuscript.

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References

1. N. Bailey, 1956. On the latent and infectious period of measles, *Biometrika* **43**(1-2): 15–22.
2. F. Ball, D. Sirl, and P. Trapman, 2010. Analysis of a stochastic SIR epidemic on a random network incorporating household structure. *Math. Biosci.*, **224**(2): 53–73.
3. A. Barbour, and G. Reinert 2013. Approximating the epidemic curve. *Electronic Journal of Probability*, **18**.
4. S. Boccaletti, V. Latora, Y. Moreno, M. Chavez, and D.-U. Hwang, 2006. Complex networks: Structure and dynamics. *Phys. Rep.*, **424**(4): 175–308.
5. M. Boguná, L. F. Lafuerza, R. Toral, and M. A. Serrano, 2014. Simulating non-markovian stochastic processes. *Phys. Rev. E*, **90**(4): 042108.
6. F. Brauer, 2008. Age-of-infection and the final size relation. *Math. Biosci. Eng.*, **5**(4): 681–690.
7. H. Brunner, Collocation methods for Volterra integral and related functional differential equations. Vol. 15. Cambridge University Press, 2004.
8. F. Cooper. Non-Markovian network epidemics, MA Thesis, 2013. www.dtc.ox.ac.uk/people/13/cooper/f/MA469ThesisFergusCooper.pdf
9. L. Decreusefond, J.-S. Dherisin, P. Moyal, and V. C. Tran, 2012. Large graph limit for an SIR process in random network with heterogeneous connectivity. *Ann. Appl. Probab.*, **22**(2), 541–575.
10. O. Diekmann, M. C. M. De Jong, and J. A. J. Metz, 1998. A deterministic epidemic model taking account of repeated contacts between the same individuals. *J. App. Probab.*, **35**: 448–462.
11. S. Janson, M. Luczak, and P. Windridge, 2014. Law of large numbers for the SIR epidemic on a random graph with given degrees. *Random Struct. Alg.*, **45**, 724–761.
12. H.-H. Jo, J. I. Perotti, K. Kaski, and J. Kertész, 2014. Analytically solvable model of spreading dynamics with non-Poissonian processes. *Phys. Rev. X*, **4**(1): 011041.
13. B. Karrer, and M. E. J. Newman, 2010. Message passing approach for general epidemic models. *Phys. Rev. E*, **82**(1): 016101.
14. M. J. Keeling and K. T. D. Eames, 2005. Networks and epidemic models. *J. Royal Soc. Interface*, **2**(4): 295–307.
15. M. J. Keeling, 1999. The effects of local spatial structure on epidemiological invasions. *Proc. R. Soc. B*, **266**(1421): 859–867.
16. M. J. Keeling and B. T. Grenfell, 2002. Understanding the persistence of measles: reconciling theory, simulation and observation. *Proc. R. Soc. B*, **269**(1489): 335–343.
17. E. Kenah, and J. M. Robins, 2007. Second look at the spread of epidemics on networks. *Phys. Rev. E*, **76**(3): 036113.
18. I.Z. Kiss, J.C. Miller, and P.L. Simon, Mathematics of epidemics on networks: from exact to approximate models. Vol. 46. IAM Series, Springer, 2017.
19. I.Z. Kiss, G. Röst, Z. Vizi, 2015. Generalization of pairwise models to non-Markovian epidemics on networks. *Phys. Rev. Lett.* **115**(7): 078701.
20. M. Laskowski, L.C. Mostago-Guidolin, A.L. Greer, J. Wu, S.M. Moghadas, 2011. The impact of demographic variables on disease spread: influenza in remote communities. *Sci. Rep.*, **1**: 105.
21. A. L. Lloyd, 2001. Realistic distributions of infectious periods in epidemic models: changing patterns of persistence and dynamics. *Theor. Pop. Biol.*, **60**(1): 59–71.
22. L. Meyers, 2007. Contact network epidemiology: Bond percolation applied to infectious disease prediction and control. *Bull. AMS*, **44**(1): 63–86,

23. B. Min, K. I. Goh, and I. M. Kim, 2013. Suppression of epidemic outbreaks with heavy-tailed contact dynamics. *EPL (Europhysics Letters)*, **103**(5): 50002.
24. M. E. J. Newman, 2002. Spread of epidemic disease on networks. *Phys. Rev. E*, **66**(1): 016128.
25. M. E. J. Newman, 2003. The structure and function of complex networks. *SIAM Review*, **45**(2): 167–256.
26. M. E. J. Newman, 2009. Random graphs with clustering. *Phys. Rev. Lett.*, **103**(5): 058701.
27. J.C. Miller, 2007. Epidemic size and probability in populations with heterogeneous infectivity and susceptibility. *Phys. Rev. E*, **76**(1): 010101(R).
28. J.C. Miller, 2008. Bounding the size and probability of epidemics on networks. *J. App. Probab.*, **45**: 498–512.
29. J.C. Miller, A. Slim, and E.M. Volz, 2012. Edge-based compartmental modelling for infectious disease spread. *J. Royal Soc. Interface*, **9**(70): 890–906.
30. J.C. Miller, and I.Z. Kiss, 2014. Epidemic spread in networks: existing methods and current challenges. *Math. Model. Nat. Phenom.*, **9**: 4–42.
31. R. Pastor-Satorras, C. Castellano, P. Van Mieghem, and A. Vespignani, 2015. Epidemic processes in complex networks. *Rev. Mod. Phys.*, **87**: 925.
32. D.A. Rand, 1999. Correlation equations and pair approximations for spatial ecologies. *Advanced ecological theory: principles and applications*, Chapter 4, 100–142.
33. P. Rattana, J.C. Miller, and I.Z. Kiss, 2014. Pairwise and edge-based models of epidemic dynamics on correlated weighted networks. *Math. Model. Nat. Phenom.*, **9**, 58–81.
34. G. Röst, Z. Vizi, I.Z. Kiss, 2016. Impact of non-Markovian recovery on network epidemics. in: Mondaini RP (ed.) *BIOMAT 2015*, World Scientific, 40–53.
35. K.J. Sharkey, C. Fernandez, K.L. Morgan, E. Peeler, M. Thrush, J.F. Turnbull, and R.G. Bowers, 2006. Pair-level approximations to the spatio-temporal dynamics of epidemics on asymmetric contact networks. *J. Math. Biol.*, **53**(1): 61–85.
36. N. Sherborne, K. B. Blyuss, and I. Z. Kiss, 2015. Dynamics of multi-stage infections on networks. *Bull. Math. Biol.*, **77**: 1909–1933.
37. N. Sherborne, K. B. Blyuss, and I. Z. Kiss, 2016. Compact pairwise models for epidemics with multiple infectious stages on degree heterogeneous and clustered networks. *J. Theor. Biol.*, **407**, 387–400.
38. N. Sherborne, J.C. Miller, K.B. Blyuss, and I.Z. Kiss, 2017. Mean-field models for non-Markovian epidemics on networks. *J. Math. Biol.* Doi: 10.1007/s00285-017-1155-0
39. P. L. Simon. and I. Z. Kiss, 2016. Super compact pairwise model for SIS epidemic on heterogeneous networks. *J. Complex Networks*, **4**(2), 187–200.
40. H. Spohn, 2012. *Large scale dynamics of interacting particles*. Springer Science & Business Media.
41. T.J. Taylor, and I.Z. Kiss 2014. Interdependency and hierarchy of exact and approximate epidemic models on networks. *J. Math. Biol.*, **69**: 182–211.
42. M. Taylor, P.L. Simon, D.M. Green, T. House and I.Z. Kiss 2012. From Markovian to pairwise epidemic models and the performance of moment closure approximations. *J. Math. Biol.*, **64**(6), 1021–1042.
43. E. Volz 2008. SIR dynamics in random networks with heterogeneous connectivity. *J. Math. Biol.*, **56**(3), 293–310.
44. E.M. Volz, J.C. Miller, A. Galvani, and L.A. Meyers, 2011. Effects of heterogeneous and clustered contact patterns on infectious disease dynamics. *PLoS Comp. Bio.*, **7**(6), e1002042.
45. R. R. Wilkinson, and K. J. Sharkey, 2014. Message passing and moment closure for susceptible-infected-recovered epidemics on finite networks. *Phys. Rev. E*, **89**: 022808.
46. R. R. Wilkinson, F. G. Ball, and K. J. Sharkey, 2017. The relationship between message passing, pairwise, Kermack-McKendrick and stochastic SIR epidemic models. *J. Math. Biol.*, 1–28, <https://doi.org/10.1007/s00285-017-1123-8>.
47. Y. Yang, M. E. Halloran, J. D. Sugimoto and I. M. Longini Jr., 2007. Detecting human-to-human transmission of avian influenza A (H5N1). *Emerg. Infect. Dis.*, **13**(9), 1348.